

2590
8/29
#8



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/982,543A

DATE: 05/02/2002

TIME: 17:23:22

Input Set : A:\CIBT-P04-523 Sequence Listing.txt
 Output Set: N:\CRF3\05022002\I982543A.raw

P6

4 <110> APPLICANT: Dijke, P.
 5 Miyazano, K.
 6 Sampath, K.
 7 Heldin, C.
 9 <120> TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL SURFACE RECEPTORS AND USES
 10 THEREFOR
 12 <130> FILE REFERENCE: CIBT-P04-543
 14 <140> CURRENT APPLICATION NUMBER: 09/982,543A
 15 <141> CURRENT FILING DATE: 2001-10-18
 17 <150> PRIOR APPLICATION NUMBER: 08/448,371
 18 <151> PRIOR FILING DATE: 1995-06-02
 20 <160> NUMBER OF SEQ ID NOS: 15
 22 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1509
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(1509)
 32 <223> OTHER INFORMATION:
 34 <400> SEQUENCE: 1

35	atg acc ttg ggc tcc ccc agg aaa ggc ctt ctg atg ctg ctg atg gcc	48
36	Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala	
37	1 5 10 15	
39	ttg gtg acc cag gga gac cct gtg aag ccg tct cgg ggc ccg ctg gtg	96
40	Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val	
41	20 25 30	
43	acc tgc acg tgt gag agc cca cat tgc aag ggg cct acc tgc cgg ggg	144
44	Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly	
45	35 40 45	
47	gcc tgg tgc aca gta gtg ctg gtg cgg gag gag ggg agg cac ccc cag	192
48	Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln	
49	50 55 60	
51	gaa cat cgg ggc tgc ggg aac ttg cac agg gag ctc tgc agg ggg cgc	240
52	Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg	
53	65 70 75 80	
55	ccc acc gag ttc gtc aac cac tac tgc tgc gac agc cac ctc tgc aac	288
56	Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn	
57	85 90 95	
59	cac aac gtg tcc ctg gtg ctg gag gcc acc caa cct cct tcg gag cag	336
60	His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln	
61	100 105 110	

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63	ccg	gga	aca	gat	ggc	cag	ctg	gcc	ctg	atc	ctg	ggc	ccc	gtg	ctg	gcc	384
64	Pro	Gly	Thr	Asp	Gly	Gln	Leu	Ala	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	
65	115						120					125					
67	ttg	ctg	gcc	ctg	gtg	gcc	ctg	ggt	gtc	ctg	ggc	ctg	tgg	cat	gtc	cga	432
68	Leu	Leu	Ala	Leu	Val	Ala	Leu	Gly	Val	Leu	Gly	Leu	Trp	His	Val	Arg	
69	130						135					140					
71	cg	agg	cag	gag	aag	cag	cgt	ggc	ctg	cac	agc	gag	ctg	gga	gag	tcc	480
72	Arg	Arg	Gln	Glu	Lys	Gln	Arg	Gly	Leu	His	Ser	Glu	Leu	Gly	Glu	Ser	
73	145						150					155			160		
75	agt	ctc	atc	ctg	aaa	gca	tct	gag	cag	ggc	gac	acg	atg	ttg	ggg	gac	528
76	Ser	Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Gly	Asp	Thr	Met	Leu	Gly	Asp	
77							165					170			175		
79	ctc	ctg	gac	agt	gac	tgc	acc	aca	ggg	agt	ggc	tca	ggg	ctc	ccc	ttc	576
80	Leu	Leu	Asp	Leu	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	
81							180					185			190		
83	ctg	gtg	cag	agg	aca	gtg	gca	cg	cag	gtt	gcc	ttg	gtg	gag	tgt	gtg	624
84	Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	
85							195					200			205		
87	gga	aaa	ggc	cgc	tat	ggc	gaa	gtg	tgg	cg	ggc	ttg	tgg	cac	gg	gag	672
88	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu	
89							210					215			220		
91	agt	gtg	gcc	gtc	aag	atc	ttc	tcc	tcg	agg	gat	gaa	cag	tcc	tgg	ttc	720
92	Ser	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	
93							225					230			235		240
95	cgg	gag	act	gag	atc	tat	aac	aca	gta	ttg	ctc	aga	cac	gac	aac	atc	768
96	Arg	Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	
97							245					250			255		
99	cta	ggc	ttc	atc	gcc	tca	gac	atg	acc	tcc	cgc	aac	tcg	agc	acg	cag	816
100	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	
101							260					265			270		
103	ctg	tgg	ctc	atc	acg	cac	tac	cac	gag	cac	ggc	tcc	ctc	tac	gac	ttt	864
104	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	
105							275					280			285		
107	ctg	cag	aga	cag	ctg	gag	ccc	cat	ctg	gct	ctg	agg	cta	gct	gtg	912	
108	Leu	Gln	Arg	Gln	Thr	Leu	Glu	Pro	His	Leu	Ala	Leu	Arg	Leu	Ala	Val	
109							290					295			300		
111	tcc	g	gc	g	c	tgc	g	cg	cac	ctg	cac	gtg	gag	atc	ttc	gg	960
112	Ser	Ala	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	
113							305					310			315		320
115	cag	ggc	aaa	cca	gcc	att	ggc	cac	cgc	gac	ttc	aag	agc	cgc	aat	gtg	1008
116	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Arg	Asn	Val	
117							325					330			335		
119	ctg	gtc	aag	agc	aac	ctg	cag	tgt	tgc	atc	gcc	gac	ctg	ggc	ctg	gct	1056
120	Leu	Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	
121							340					345			350		
123	gtg	atg	cac	tca	cag	ggc	agc	gat	tac	ctg	gac	atc	ggc	aac	aac	ccg	1104
124	Val	Met	His	Ser	Gln	Gly	Ser	Asp	Tyr	Leu	Asp	Ile	Gly	Asn	Asn	Pro	
125							355					360			365		
127	aga	gtg	ggc	acc	aag	cgg	tac	atg	gca	ccc	gag	gtg	ctg	gac	gag	cag	1152

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128 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
 129 370 375 380
 131 atc cgc acg gac tgc ttt gag tcc tac aag tgg act gac atc tgg gcc 1200
 132 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
 133 385 390 395 400
 135 ttt ggc ctg gtg ctg tgg gag att gcc cgc cgg acc atc gtg aat ggc 1248
 136 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
 137 405 410 415
 139 atc gtg gag gac tat aga cca ccc ttc tat gat gtg gtg ccc aat gac 1296
 140 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
 141 420 425 430
 143 ccc agc ttt gag gac atg aag aag gtg gtg tgt gtg gat cag cag acc 1344
 144 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
 145 435 440 445
 147 ccc acc atc cct aac cgg ctg gct gca gac ccc gtc ctc tca ggc cta 1392
 148 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
 149 450 455 460
 151 gct cag atg atg cgg gag tgc tgg tac cca aac ccc tct gcc cga ctc 1440
 152 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
 153 465 470 475 480
 155 acc gcg ctg cgg atc aag aag aca cta caa aaa att agc aac agt cca 1488
 156 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
 157 485 490 495
 159 gag aag cct aaa gtg att caa 1509
 160 Glu Lys Pro Lys Val Ile Gln
 161 500
 163 <210> SEQ ID NO: 2
 164 <211> LENGTH: 503
 165 <212> TYPE: PRT
 166 <213> ORGANISM: Homo sapiens
 168 <400> SEQUENCE: 2
 169 Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
 170 1 5 10 15
 172 Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
 173 20 25 30
 175 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
 176 35 40 45
 178 Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
 179 50 55 60
 181 Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
 182 65 70 75 80
 184 Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
 185 85 90 95
 187 His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
 188 100 105 110
 190 Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
 191 115 120 125
 193 Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
 194 130 135 140

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196 Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
 197 145 150 155 160
 199 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
 200 165 170 175
 202 Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
 203 180 185 190
 205 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
 206 195 200 205
 208 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
 209 210 215 220
 211 Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
 212 225 230 235 240
 214 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
 215 245 250 255
 217 Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
 218 260 265 270
 220 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
 221 275 280 285
 223 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
 224 290 295 300
 226 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
 227 305 310 315 320
 229 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
 230 325 330 335
 232 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
 233 340 345 350
 235 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
 236 355 360 365
 238 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
 239 370 375 380
 241 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
 242 385 390 395 400
 244 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
 245 405 410 415
 247 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
 248 420 425 430
 250 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
 251 435 440 445
 253 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
 254 450 455 460
 256 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
 257 465 470 475 480
 259 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
 260 485 490 495
 262 Glu Lys Pro Lys Val Ile Gln
 263 500
 265 <210> SEQ ID NO: 3
 266 <211> LENGTH: 2724
 267 <212> TYPE: DNA

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 Output Set: N:\CRF3\05022002\I982543A.raw

268 <213> ORGANISM: Homo sapiens
 270 <220> FEATURE:
 271 <221> NAME/KEY: CDS
 272 <222> LOCATION: (104)..(1633)
 273 <223> OTHER INFORMATION:
 275 <400> SEQUENCE: 3
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 278 gactgtggc agatgtgacc aagagcctgc attaagttgt aca atg gta gat gga 115
 279 Met Val Asp Gly
 280 1
 282 gtg atg att ctt cct gtg ctt atc atg att gct ctc ccc tcc cct agt 163
 283 Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser
 284 5 10 15 20
 286 atg gaa gat gag aag ccc aag gtc aac ccc aaa ctc tac atg tgt gtg 211
 287 Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val
 288 25 30 35
 290 tgt gaa ggt ctc tcc tgc ggt aat gag gac cac tgt gaa ggc cag cag 259
 291 Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln
 292 40 45 50
 294 tgc ttt tcc tca ctg agc atc aac gat ggc ttc cac gtc tac cag aaa 307
 295 Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys
 296 55 60 65
 298 ggc tgc ttc cag gtt tat gag cag gga aag atg acc tgt aag acc ccg 355
 299 Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro
 300 70 75 80
 302 ccg tcc cct ggc caa gct gtg gag tgc tgc caa ggg gac tgg tgt aac 403
 303 Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp Trp Cys Asn
 304 85 90 95 100
 306 agg aac atc acg gcc cag ctg ccc act aaa gga aaa tcc ttc cct gga 451
 307 Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys Ser Phe Pro Gly
 308 105 110 115
 310 aca cag aat ttc cac ttg gag gtt ggc ctc att att ctc tct gta gtg 499
 311 Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu Ser Val Val
 312 120 125 130
 314 ttc gca gta tgt ctt tta gcc tgc ctg ctg gga gtt gct ctc cga aaa 547
 315 Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys
 316 135 140 145
 318 ttt aaa agg cgc aac caa gaa cgc ctc aat ccc cga gac gtg gag tat 595
 319 Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr
 320 150 155 160
 322 ggc act atc gaa ggg ctc atc acc acc aat gtt gga gac agc act tta 643
 323 Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu
 324 165 170 175 180
 326 gca gat tta ttg gat cat tcg tgt aca tca gga agt ggc tct ggt ctt 691
 327 Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu
 328 185 190 195
 330 cct ttt ctg gta caa aga aca gtg gct cgc cag att aca ctg ttg gag 739
 331 Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu
 332 200 205 210

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 2,3,9,11,16,19,23,26,35,39,41,50,52,56,57,58,60,61,65,71

Seq#:11; Xaa Pos. 73,75,80,82,84,87,89,91,97

Seq#:12; N Pos. 20